TITLE ME Scoucning

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nessed (	a unaet	21000 D	y me,	Date	[	nvented by	Date
n o o o o o o	0 111						To Page
		19221	Humai	05/00	pointin	mRNA	99 % (279/281)
.223		9220				NA clone 53126 3'	97% (88/90)
222		9219				II mRNA	59% (98/109)
221		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~			- 1.	T NA	
720		9217	Human	ncph:	ropon	in mRNA	99 % (275/250)
719		<i></i>	. 1	······		N.A	
218	·	19215	Humai	n glyco	protei	1 mBNA	68 % (178/258)
		19214				mRNA Dua	99 % (281/283)
217						divator precurso (human)	96% (236/244)
216		19213	Ga	1 nepni	10 po.n.	in mRNA	100% (283/283)
215		M212				dlagenase mRNA	94 % (779/241)
214		19211					
213		19210	Lecith	به، ده	100	of cityl bransferase	100% (283/243)
212		19709				intron 16, partial seq.	75% (48/129)
MØ 211	MC	19705	Homo	sapicas	c DN	13' end	94 % (245/760)
	X						
	730	0.0554	0.0842 1.39	1.8198	0.6174		and the second s
	2 <b>2</b> 9	0.0522 0.0557	0.0018 <b>1.31</b> 0.0084 <b>1.39</b>	1.6699 1.5783	9,6998 0,6958	Security of the contract of th	
	2 <b>77</b>	0.0357 6.0853	0.0227 .69	1.5720	0.6061		Production regarded and administration of the control of the contr
	226	0.0232	0.0150 .59	1,555 1,555 1,555	0.6334		
	274 225	0.0218 0.0380	0.0158 <b>.55</b> 0.0249 <b>.95</b>	1,4010 1,5280	0,7136 6,6648		The contract contract the same of the contract
	553	0.0271	0.0187 · <b>69</b>	1,4499	0,6900		the brain that week new the purposes are arranged and the second section in the second section in the second section is a second section of the second section
	212	0.0486	0.0349 1.72	1,3536	0.7174		•
	2 <b>2</b> 0 2 <b>21</b>	0.0495 0.0438	0.0288 1-24 0.0292 1-22	1.7194 1.8709	0.5818 6.5988		
	219	0.0525	0.0299 1.31	1.7548	0.5700		the second with the second or comments to the second of th
	218	f.0382	0.0218 .96 0.0218 .96	1,7597	6.5654		
	216 217	0.0587 0.0519	0.0075 L47 0.0089 1.30	1.8765 1.7986	0.8542 0.8577	(Please provide OD260 and insert size)	
	715	(,0378	(,( <u>())</u> 5 .45	1.8549	0.5450	Names of Sample(s): MØ 211-230 (Please provide OU260 and insert size)	to samples) (OD us on late)
	214	0.0521	(,3303 1.30	1,7230	0.5569 0.5304	Vector: pRe/(MV Host:	soi Clones 20
	213	0.0471 0.0412	0.0255 1 <b>.18</b> 0.0227 1 <b>.03</b>	1.8 <b>43</b> 0 1.8151	0.5429	At a constant	pProject: #e
	211	0.0368	9.0235 <b>.</b> 92	113611	0.8343	Requested by Jaron Smelh	Data
·		260.0 ne	230.0 At	266.0 m	34.4 m	DNA SEQUENC	ING REQUEST Department
	Sangle	iks	<b>£</b> ist	280.4 m	221.4.51	,	
							enderando españo. A que a minima en entre provincia en el el esta de la compa

mc19215 JHSP6 primer MO218 Lane 28

Model 373A Version 2.0.1A

Signal G:331 A:158 T:92 C:81 DyeTerminator{AnyPrimer} 197 MATRIX FILE Points 441 to 3936 Base 1: 441

Spacing: 0.0

LON / WANTEN WENT WIND IN

## cc:Mail for: heather pearson

Subject: No subject given P Forwarded: JEFF GARDIN

To: Heather Pearson

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To: Aaron_Smith_at_ICOS-Science@icos.com
 Subject: Re: 19215
 gb | M80927 | HUMHA3G
                   Human glycoprotein mRNA, complete cds.
                                                      572
                                                          4.8e-40
 gb U19900 SSU19900
                   Sus scrofa 38kDa heparin-binding gly...
                                                      546
                                                          7.1e-38
 gb R55530 R55530
                   yj79c12.rl Homo sapiens cDNA clone 1...
                                                      368
                                                          2.3e-21
 dbj | D32218 | HAMOSG
                   Hamster mRNA for oviduct-specific gl...
                                                      271
                                                          8.1e-13
                   Human oviductal glycoprotein mRNA, c...
 gb U09550 HSU09550
                                                          1.8e-12
                                                      267
 gb U17988 | OAU17988
                   Ovis aries 92kD oestrus-associated o...
                                                      235
                                                          9.0e-10
 dbj|D16639|BOV95BOGP Bovine mRNA for 95 kDa oviduct-speci...
                                                      217
                                                          3.1e-08
 gb U15048 MAU15048
                  Mesocricetus auratus oviductin mRNA,...
                                                      211
                                                          1.0e-07
 gb R03212 R03212
                  pk05a03.s1 Caenorhabditis briggsae c...
                                                      201
                                                          4.5e-07
 gb U13646 CELZK783
                  Caenorhabditis elegans cosmid ZK783.
                                                      129
                                                         0.58
 gb T92100 T92100
                  ye01h11.r1 Homo sapiens cDNA clone 1...
                                                      123 0.91
 >gb|M80927|HUMHA3G Human glycoprotein mRNA, complete cds.
           Length = 1741
  Plus Strand HSPs:
 Score = 572 (158.1 bits), Expect = 4.8e-40, P = 4.8e-40
 Identities = 178/258 (68%), Positives = 178/258 (68%), Strand = Plus / Plus
         24 CAGGTTTCATGGTCCTGCTGATGATCCCATGGGGCTCTGCTGCAAAACTGGTCTGCTACT 83
                  Sbjct:
         94 CAGGCTTTGTGGTCCTGGTGCTCCAGTGCTGCTCTGCATACAAACTGGTCTGCTACT 153
         84 TCACCAACTGGGCCCAGTACAGACAGGGGGGGGGGGGTCGCTTCCTGCCCAAGGACTTGGACC 143
Query:
            111 1 1 11 1 1 1 1 1 1 1 1 1
Sbjct:
        154 ACACCAGCTGGTCCCAGTACCGGGAAGGCGATGGGAGCTGCTTCCCAGATGCCCTTGACC 213
        Query:
               Sbjct:
        214 GCTTCCTCTGTACCCACATCATCTACAGCTTTGCCAATATAAGCAACGATCACATCGACA 273
Query:
        204 CCACTGAGTGGAATGACGAGACTCTCTACCAGGAGTTCAATGGCCTGAAGAAGATGAATC 263
               Sbjct:
        Query:
        264 CCAAGCTGAAGACCCTGT 281
            Sbict:
        334 CCAACCTGAAGACTCTCT 351
>gb|U19900|SSU19900 Sus scrofa 38kDa heparin-binding glycoprotein mRNA,
          complete cds. >emb|Z47803|SSGP38KD S.scrofa 38kDa heparin-binding
          glycoprotein.
          Length = 1733
  Plus Strand HSPs:
 Score = 546 (150.9 bits), Expect = 7.1e-38, P = 7.1e-38
 Identities = 184/278 (66%), Positives = 184/278 (66%), Strand = Plus / Plus
         2 ATGGTGCGGTCTGTGGCCTGGGCAGGTTTCATGGTCCTGCTGATGATCCCATGGGGCTCT 61
Query:
                            1 1111111
           HHI
                     11111
                                     Sbjct:
        67 ATGGGTCTGAGGGTGGCTCAGACAGGTTTTGTGGCCCTGGTGCTGCTCCAGAGCTGTGCT 126
Query:
```

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1

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1

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